

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

```
Run on: April 4, 2003, 22:43:10 ; Search time 4493 Seconds
        (without alignments)
        1192.889 Million cell updates/sec
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Title: US-09-847-081B-1
 Perfect score: 1728
 Sequence: 1 agaaaccagaaagacac.....tcataaacctcaagtga 1728

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_ma:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
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13: gb_un:*
14: gb_vl:*
15: en_ba:*
16: en_fun:*
17: en_hum:*
18: en_in:*
19: en_mu:*
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21: en_or:*
22: en_ov:*
23: en_pat:*
24: en_ph:*
25: en_pl:*
26: en_ro:*
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30: en_htg_hum:*
31: en_htg_inv:*
32: en_htg_other:*
33: en_htg_pln:*
34: en_htg_pln:*
35: en_htg_rod:*
36: en_htg_mam:*
37: en_htg_vrt:*
38: en_sy:*
39: en_hgo_hum:*
40: en_hgo_mus:*
41: en_hgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	Match				
1	862.8	49.9	1119	8	TOMPSY2A	L23424	Lycoopersico
2	856.2	49.5	1295	8	CAPSY1	68017	C annuus ps
3	847.6	49.1	1786	8	TOMCBBE	M84744	Tomato phyt
4	842	48.7	1846	6	A021360	L21360	L. esculentum
5	842	48.7	1846	6	AR007503	L21360	L. esculentum
6	829.8	48.0	1614	8	LERIPE	Y0521	Tomato frui
7	811.2	46.9	1239	6	A68204	Sequence 2	A68204
8	811.2	46.9	1239	6	AR156064	Sequence 2	AR156064
9	811.2	46.9	1239	6	BD005486	Enhanceme	BD005486
10	772	44.7	1355	8	LERYGTOM5	X67144	L. esculentum
11	696.8	40.3	1506	8	AF220218	Citrus un	AF220218
12	696.8	40.3	1689	8	AB037975	Citrus un	AB037975
13	692.8	40.1	1773	8	AF152892	Citrus x	AF152892
14	692.4	40.1	2868	6	E15683	Gentiana l	E15683
15	678.4	39.3	1921	6	E15681	Gentiana lu	E15681
16	670.4	38.8	2085	6	E15680	Gentiana lu	E15680
17	653.4	37.8	1932	6	E15682	Gentiana lu	E15682
18	650.6	37.7	1637	8	HANX08385	Helianthu	AJ308385
19	645.8	37.4	1598	8	HANX04825	Helianthu	AJ304825
20	644.2	37.3	1371	6	AF251015	Tagetes e	AF251015
21	643.2	37.2	1712	6	A48337	Tagetes e	A48337
22	643.2	37.2	1576	8	CMPSY1MR	Sequence 1	CMPSY1MR
23	625.4	36.2	1376	8	AY099482	C. melo PSY1	237543
24	591.6	34.2	1548	8	NPPSY	Tagetes e	AY099482
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26	578.4	33.5	1853	8	AY056287	Arabidops	AY085365
27	563.8	32.6	1769	8	ATPHPHYSYN	Arabidops	AY056287
28	514.2	29.8	1538	8	AB032797	Arabidopsis	L25812
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30	463.8	26.8	1060	8	AY024350	Sequence	AX350858
31	426.4	24.7	686	8	AF158024	Oryza sat	AY024350
32	425	24.6	681	8	AF196963	Tagetes e	AF158024
33	415.2	24.0	1239	6	A68203	Bixa orel	AF196963
34	415.2	24.0	1239	6	AR156063	Sequence 1	A68203
35	415.2	24.0	1239	6	BD005485	Sequence	AR156063
36	362.2	21.0	4073	8	LERSPS	Enhanceme	BD005485
37	301.6	17.5	1278	8	DB091900	L. esculentum	X60440
38	282.6	16.4	1859	8	AF305430	Dunalietia	U91900
39	257.4	14.9	343550	1	AB003587	Haematoco	AF305430
40	252	14.6	1081	1	AP001384	Nostoc sp	AB003587
41	246.2	14.2	629	8	AY078162	Spirulina	AB001384
42	245	14.2	1465	1	SSPPHYSYN	Oryza sat	AY078162
43	245	14.2	119184	1	D90909	Synechocyst	X63172
44	230.2	13.3	301200	8	AP005374	Synechocyst	D90909
45	222.2	12.9	3707	8	LEGTOM5	Thermosyn	AP005374

ALIGNMENTS

RESULT 1	
TOMPSY2A	
LOCUS	1119 bp mRNA linear PLN 04-JAN-1994
DEFINITION	Lycopersicon esculentum phytoene synthase (PSY2) mRNA, complete cds.
ACCESSION	L23424
VERSION	L23424.1 GI:437019
KEYWORDS	phytoene synthase.
SOURCE	Lycopersicon esculentum Mature leaf cdNA to mRNA.
ORGANISM	Lycopersicon esculentum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
REFERENCE	lycopersicon. 1 (bases 1 to 1119)

AUTHORS Bartley G.E. and Scolnik, P.A.
 TITLE cDNA cloning, expression during development, and genome mapping of
 PSY2, a second tomato gene encoding phytoene synthase
 J. Biol. Chem. 268 (34), 25718-25721 (1993)
 MEDLINE 94064645
 PUBMED 8245008

FEATURES

Location/Qualifiers

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/organism="Lycopersicon esculentum"

/db_xref="taxon:4081"

/tissue_type="Leaf"

/dev_stage="Mature leaf"

1..1119

/gene="PSY2"

1..934

/partial

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/note="RT-PCR product"

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/partial

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/note="approximate location"

mat_peptide

77..931

/product="phytoene synthase"

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ORIGIN

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 Best Local Similarity .89.0%; Pred. No. 1.1e-202;
 Matches 984; Conservative 0; Mismatches 102; Indels 20; Gaps 4;

QY 633 GAAGCCGGATATGTTGTTCCAGGGAATTTGGCTTGTTCAGTGAAGCATATCATGCTTG 692
 DB 1 GGATCCGGATATGTTCTCCGGTATTTGGCTTGTTCAGTGAAGCATATCATGCTTG 60
 QY 693 TGGCAGATATGTCAGAGATATCAAGACATTTTACTTAGGAACCAAGCTAATGACCC 752
 DB 61 TGCGAAGTATGTCAGAGATATCAAGACATTTTACTTAGGAACCAAGCTAATGACCTC 120
 QY 753 AGAGAGAAGAGAGCTATCTGGCAATATATGTTGGTGCAGGAGAACGGATGCTTGT 812
 DB 121 AGACAGAAGAGAGCTATCTGGCAATATATGTTGGTGCAGGAGAACGGATGCTTGT 180
 QY 813 TGATGGCCCTAATGCATCCACATAACTCCGCAAGCTTTAGATAGTGGGAGACCAAGCT 872
 DB 181 TGATGGCCCTAATGCATCCACATAACTCCGCAAGCTTTAGATAGTGGGAGACCAAGCT 240
 QY 873 GGAAGATATTTTCAAGTGGGGCCATTTGATATGCTTGATGCTTTTATCCGATCTGT 932
 DB 241 GGAAGATATTTTCAAGTGGGGCCATTTGATATGCTTGATGCTTTTATCCGATCTGT 300
 QY 933 CTCAGATTTCCGTTGATATTCAGCATTCAGCATATGATTTGAAGGAATGCGTATGA 992
 DB 301 TTCAGATTTCCGTTGATATTCAGCATTCAGCATATGATTTGAAGGAATGCGTATGA 360
 QY 993 CTTGTGGAATCCAGATACAAACACTTTCGATGAGCTATATCTTATGTTACTATGTC 1052
 DB 361 CTTGTGGAATCCAGATACAAACACTTTCGATGAGCTATATCTTATGTTACTATGTC 420
 QY 1053 TGGTACTGTAGGATGATAGTGTCCAGTATGGTATTTGACCTGAATCAAGGCAAC 1112
 DB 421 TGGTACTGTAGGATGATAGTGTCCAGTATGGTATTTGACCTGAATCAAGGCAAC 480

QY 1113 AACAGAGAGTGTATATAATCTCTCTTTGGCTTTAGGCTTGCATAATCAACCAATAT 1172
 DB 481 GACAGAGAGTGTATATAATCGAGCTTTGGCTTTAGGCTTGCATAATCAACCAATAT 540
 QY 1173 ACTCAGAGATGTAGGAGAGATGCCAGAGAGGAGAGATATCTTGGCTCAAGATGAAT 1232
 DB 541 ACTCAGAGATGTAGGAGAGATGCCAGAGAGGAGAGATATCTTGGCTCAAGATGAAT 600
 QY 1233 AGCAGAGGAGGCTCTCCGACGAGACATATTTGCTTGGAGAGTGAAGTGAAGTGGAG 1292
 DB 601 AGCAGAGGAGGCTCTCCGATGAGACATATTTGCTTGGAGAGTGAAGTGAAGTGGAG 660
 QY 1293 GAACCTTTATGAAGAAACAATTCAGAGGCGAGGAAATTTCTTGTATGATGAGTGAAGAG 1352
 DB 661 AATCTTTATGAAGAAACAATTCAGAGGCGAGGAAATTTCTTGTATGAGGAGAGAGAG 720
 QY 1353 TGTACAGAACTGACTCTCTAGTAGAGTGCCTTGTAAACAGCGCTGCTTGTATGTCG 1412
 DB 721 TGTACAGAACTGACTCTCTAGTAGAGTGCCTTGTAAACAGCGCTGCTTGTATGTCG 780
 QY 1413 CAAGATATTGGAGAGATTGAAGCCAGACTACAAACAACCTTCAAGAGGCGCTTATGT 1472
 DB 781 CAAGATATTGGAGAGATTGAAGCCAGACTACAAACAACCTTCAAGAGGCGCTTATGT 840
 QY 1473 TAGCAGCCAAAGAGCTTCTACCTTGGCCATTTGCTTGAAGAAATCTCTTGTGCCCC 1532
 DB 841 GAGCAAGCCAAAGAGCTTCTACCTTGGCCATTTGCTTGAAGAAATCTCTTGTGCCCC 900
 QY 1533 TAATAGAACTTCTCTCCACTAGCAAGAGATGAATCAAGTAGTTGAGT-----CAA 1584
 DB 901 TAATAGAACTTCTCTCCACTAGCAAGAGATGAATCAAGTAGTTGAGT-----CAA 1584
 QY 1585 TGAGTATTATACACTAAAGAA---ACTCAGGTACTTCTAAATGAGATATCTTTTGCCTAAA 1641
 DB 961 GCCTATATACACTAAAGAAACAGGCTACTTAATCTAAATGAGCTATC-TTGTGCTACA 1019
 QY 1642 TGTG-----TATCATCAAAAGTAGATTGTAATTCATATGACAAATCTCTTGTGTAGA 1693
 DB 1020 TGTGTTTCATCATATCATTAATGAGTAGATTGTAATTCATATGACAAATCTCTTGTGTAGA 1079
 QY 1694 ATATTTTCCACACTCATCAAAACC 1719
 DB 1080 TTAATGTGCTTCACTTTCACACTC 1105

RESULT 2

CAPSY1

LOCUS

DEFINITION

X68017

VERSION

X68017.1

KEYWORDS

phytoene synthase

SOURCE

ORGANISM

CAPSY1

C. annum

1295 bp

mrna

linear

PLN 05-FEB-1994

C. annum

psyl

mrna

for phytoene synthase.

X68017.1

GI:433993

phytoene synthase

Capsicum annuum

Capsicum annuum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.

Kuntz, M.

Direct Submission

Submitted (30-JUL-1992)

M. Kuntz, Inst. de Biologie Molec. des Plantes, 12 rue du Général Zimmer, 67084 Strasbourg, FRANCE

Plantes, 12 rue du Général Zimmer, 67084 Strasbourg, FRANCE

2 (bases 1 to 1295)

Romer, S., Hugueney, P., Bouvier, F., Camara, B. and Kuntz, M.

Expression of the genes encoding the early carotenoid biosynthetic enzymes in Capsicum annuum

Biochem. Biophys. Res. Commun. 196 (3), 1414-1421 (1993)

94071905

PUBMED

FEATURES

Location/Qualifiers

1..1295

/organism="Capsicum annuum"

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/dev_stage="ripening fruits"
1. 1260
/gene="psyl"
1. 1260
CDS
/gene="psyl"
/note="subunit structure monomer"
/codon_start=1
/product="phytoene synthase"
/protein_id="CAA48155.1"
/db_xref="GI:43394"
/db_xref="SWISS-PROT:P37272"
/translation="MSVALLWVSPDVSNGTFLVSVREGNRFIDSGRRNLACNER
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AIWAIWVCRERDELVDGNASHITPAALDRWEDLEDFSCRPDMLDAALSDTVSK
FPYDIOPFRDMIEGRMDLKSRYRNFDELILYCYTVAGTVGLMSPIMGIAPEKAT
TESVINAALGIANQLTILRDVGEDARRGVLYLPQDELAQGLSDEDFIAGRVDK
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BASE COUNT 379 a 219 c 361 g 336 t
ORIGIN

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Query Match 49.5%; Score 856.2; DB 8; Length 1295;
Best Local Similarity 81.5%; Pred. No. 4.8e-201;
Matches 1057; Conservative 0; Mismatches 198; Indels 42; Gaps 4;

QY 250 ATGTCCTGCTTGTGGTGGTGTTCCTCCACCTCCGAGTCTCGAATGGGACAGGA 309
Db 1 ATGTCCTGCTTGTGGTGGTGTTCCTCCACCTCCGAGTCTCGAATGGGACAGGA 57

QY 310 TTGTTGGATTGAGTCCGAGAGAAACCGGCTCTTTGTATCATCCAGGTTCCCTAGTCGA 369
Db 58 TTCTTGGTATCCGTTCTGAGGAAACCGGATTTTGTATCGTCGGGG----- 105

QY 370 GATAGGAATTTGATGGGAATCAAGA---AGGTGGGAGACAAAGTGGGAAT 426
Db 106 CGTAGGAATTTGGCGTGCAATGAGAGAATCAAGAGAGAGGTGGGAAACAAAGTGGAGT 165

QY 427 TTTGGCTTTAATGCTGATCCAGATATTCATGCTTGGTGGATCAAGACTGAAAG 486
Db 166 TTTGG-----TTCTTACTTGGGAGGAGCAACAACTGGAAGT 201

QY 487 GGAAGCACTTCTCTACAGTCCAGTTGGTGGCTAGCCAGCTGGAGAAATGACTGTG 546
Db 202 GGACGGAATTTCTGATCGTTCTGCTATGCTGGCTACTCGGCTGGAGAAATGACGATG 261

QY 547 TCATCAGAGAAAAGGTGTATGATGTGGTATTAAGCAGGCGAGCTTTAGTGAAGAGCAG 606
Db 262 TCATCAGAACGGATGATGATGTGGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 321

QY 607 CTGAGACTACCGATGATTAGAGTGAAGCCGATATTTGTTCCAGGGAATTTGGGC 666
Db 322 CTGAGACTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 381

QY 667 TTGTTGAGTGAAGCATATGATGCTTGTGGGCAAGTATGTCAGAGTATGCAAGACATTT 726
Db 382 TTGTTGAGTGAAGCATATGATGCTTGTGGGCAAGTATGTCAGAGTATGCAAGACATTT 741

QY 727 TACTTAGGAACCAAGCTAATGACCCAGAGAGAGAGAGATCTCTGGCCTAATATGATG 786
Db 442 TACTTAGGAACCAAGCTAATGACCTCCGAGAGAGAGAGAGATCTCTGGCCTAATATG 501

QY 787 TGGTGCAGGAACCGATGATGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 846
Db 502 TGGTGCAGGAACCGATGATGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 561

QY 847 GCTTTAGATAGTGGGAGACCGAGCTGGAAGATATTTTCACTGGGCGCCATTTGATATG 906
Db 562 GCTTTAGATAGTGGGAGACCGAGCTGGAAGATATTTTCACTGGGCGCCATTTGATATG 621

QY 907 CTTGATGCTGCTTATCCGATACCTGCTCCAGATTTCTCTGTTGATATTCAGCCATTCAGA 966

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Db 682 GATATGATTGAAGGAATGCGTATGAGTCTGTGGAAATCCAGATACAAATCTTCGACGA 741
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Db 742 CTATACCTATATTTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 801
QY 1087 GGATTCACCTGATCAAGGCAACACAGAGAGTGTATATATGCTGCTTGGCTTTA 1146
Db 802 GGATTCACCTGATCAAGGCAACACAGAGAGTGTATATATGCTGCTTGGCTTTG 861
QY 1147 GGCTTCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1206
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QY 1207 AGATATATCTTGCCTCAAGATGAATTAGCAGCAGGCGCTCTCCGAGCAAGACATATTT 1266
Db 922 AGATCTATTTGCCTCAAGATGAATTAGCAGCAGGCTCTATCCGACGAAGACATATTT 981
QY 1267 GCTGGAAGAGTACTGATAGTGGAGGAATTTATGAAGAAACAAATTCAGAGGCGGAGG 1326
Db 982 GCTGGAAGAGTACTGATAGTGGAGGAATTTATGAAGAAACAAATTCAGAGGCGGAGG 1041
QY 1327 AATCTCTTGGATGAGTCAAGAAAGGTTCTACAGAACTGGACTCTGCTAGTAGTGGCT 1386
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QY 1387 GTGTTAAACAGCGCTGCTGTTGATCGCAAGATATTGGACGAGATTGAAGCCAAACGACTAC 1446
Db 1102 GTGTTGCACTCTGCTGTTGATCGCGAGGATCTGGACGAGATCGAAGCCAAACGACTAC 1161
QY 1447 AACAACTTCAAGAGGCGCTTATGTTAGCAAGCCAAAGAGCTTCTCACCTTGGCCATTT 1506
Db 1162 AACAACTTCAAGAGAGAGCTTATGTGAGCAACCAAGAAAGTGTGATTGCAATACCTATT 1221
QY 1507 GCTTATCCAAATCTCTTGTGCCCCCTTAATAGAATT 1543
Db 1222 GCATATCAAAATCTCTTGTGCGCTTCTACAAGAACAT 1258

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RESULT 3
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LOCUS
DEFINITION
ACCESSION
VERSION
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AUTHORS
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JOURNAL
MEDLINE
PUBMED
FEATURES
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314. 1552
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TOMCBPE
Tomato phytoene synthase mRNA, complete cds.
1786 bp mRNA linear PLN 27-APR-1993
M84744.1 GI:170415
carotenoid biosynthesis; phytoene synthetase.
Lycopersicon esculentum (library: Clontech fruit cDNA) breaker
fruit stage fruit cDNA to mRNA.
Lycopersicon esculentum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 1786)
Bartley,G.E., Viitanen,P.V., Bacot,K.O. and Scolnik,P.A.
A tomato gene expressed during fruit ripening encodes an enzyme of
the carotenoid biosynthesis pathway
J. Biol. Chem. 267 (8), 5036-5039 (1992)
92184738
1544888

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Query Match 49.1%; Score 847.6; DB 8; Length 1786;
Best Local Similarity 77.6%; Pred. No. 6.3e-199;
Matches 1136; Conservative 0; Mismatches 249; Indels 79; Gaps 6;

QY 101 TATAATCGTTCAATTAAGTGGATAGACTCTAGTGGATATCTAC---AAGTATTGGTTTTT 157
DB 166 TAAATTTGTTGAGGTGGAAATATCTCTAGTGGGAATCTACTAGGAGTAATTTATTTT 225
QY 158 TGATAAATAGGCTGAGGTGAGAGGTACATAAAGAAAGACAAAACTTGGGAATTGT 217
DB 226 CTATAAACTAAGTAAAGTTTGGAGGTGACA-AAAGAAAGACAAATCTTGGNAATTGT 284
QY 218 TTTAGACACCGAGGTTCTTGTTCATGAGCATGTCGTGTTGCTTTGTTGGTTGTTT 277
DB 285 TTTAGACAACCAAGGT---TTTCTTGCTCAGAAATGCTGTTGCTTTGTTATGGTTGTTT 341
QY 278 CTCCACTCCGAGGCTCCGAATGGGACAGATGTTGGATTTCAGTCCGAGAGGAAC 337
DB 342 CTC---CTTGTGAGCTTCAATGGGACAGTTTCATGGAATCAGTCCGGGAGGAAC 398
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DB 399 GTTTTTTTGATTCATCAGG-----CATAGGAATTTGGTGTCCTCAATGAGAGAA 446
QY 398 TCAAGAAGGTGGGACAAAGGTGGAAATTTTGCTCTTTTAAATGCTGATCCAAGATATT 457
DB 447 TCAATAGAGGT----- 457
QY 458 CATGCTTTGGTGGATCAGAACTGAAAGGAGCACTTTCTCTGTACAGTCCAGTTGG 517
DB 458 -----GGTGGAAACCAACTAATAATGGACGGAAATTTTCTGTACGGTCTGCTATTT 509
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DB 510 TGGCTACTCCATCTGGAGACGGACGATGACATCGGACAGATGGTCTATGATGTGGTTT 569
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QY 638 CGGATATTGTTGCCAGGAAATTTGGCTTTGTTGAGTGAAGCATATGATCGTTTGGCG 697
DB 630 CGGATATACCTATTTCGGGGAATTTGGCTTTGTTGAGTGAAGCATATGATAGTGTGGTG 689
QY 698 AAGTATGTGAGAGTATGCAAGACATTTTACTTTAGGAACCAAGCTAATGACCCCGCAGAGA 757
DB 690 AAGTATGTGAGAGTATGCAAGACGTTTAACTTTAGGAATATGCTAATGACTCCCGAGA 749
QY 758 GAAGAAGAGCTATCTGGGCAATATATGTTGGTGCAGGAGAACGGATGAGCTTGTGATG 817
DB 750 GAAGAAGGGCTATCTGGGCAATATATGTTGGTGCAGGAGAACGATGAACTTGTGATG 809
QY 818 GCCCTATGATCCCATACATCCCGAAGCTTTAGATAGTGGGAGACCGAGCTGGAAG 877
DB 810 GCCCAAGAGCATATATATACCCCGAGCCTTAGATAGTGGGAAATAGGCTAGAAG 869
QY 878 ATATTTTTCAGTGGCGGCCCATTTGATATGCTGATGCTGCTTATCCGATACTGCTCCA 937
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DB 870 ATGTTTCAATGGCGGCCCATTTGACATGCTCGATGGTGTCTTGTCCGATACAGATTCTTA 929
QY 938 GATTTCCTGTTGATATTCAGCCATTTCAGAGATATGATTGAAGGAATCGGTATGACTTGT 997
DB 930 ACITTCAGTGTGATATTCAGCCATTTCAGAGATATGATTGAAGGAATCGGTATGACTTGA 989
QY 998 GGAATCCAGATCAAAACTTTTCGATGAGCTATATCTCTATTGTTACTATGTTGCTCGTGA 1057
DB 990 GAAATTCGAGATCAAAACTTCGAGCACTATACCTTTATTGTTATTATGTTGCTCGTGA 1049
QY 1058 CTCTAGGATGATGAGTGTTCCTAGTTATGTTGATGTTGACCTGAATCAAGGCAACAACAG 1117
DB 1050 CGTTGGTTCGATGAGTGTTCCTAATATGTTGATGTTGCGCTGAATCAAGGCAACAACAG 1109
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DB 1110 AGAGCGTATATAATGCTGCTTTGGCTCTGGGATCGCAAAATCAATTAACATACTCA 1169
QY 1178 GAGATGTAGGAGAGATGCCAGAGAGGAGAGATATCTTGCCTCAAGATGAATTAGCAC 1237
DB 1170 GAGATGTGGAGAGATGCCAGAGAGGAGAGTCTACTTGCCTCAAGATGAATTAGCAC 1229
QY 1238 AGCAGGCGCTCTCCGACGAGACATATTTGCTGGAAGAGTGACTGATAAGTGGAGGAAC 1297
DB 1230 AGCAGGCTCTATCCGATGAAGATATTTCTGCTGGAAGGTGACCGATGAATGGAGATCT 1289
QY 1298 TTATGAAGAAACAAATTCAGAGGGCGAGGAAATTTCTTTGATGATCAGAGAAAGGTGCA 1357
DB 1290 TTATGAAGAAACAAATACATAGGCAAGAAAGTTCTTTGATGAGGACAGAGAAAGCGTGA 1349
QY 1358 CAGAACTGGACTCTGCTAGTAGATGGCTGTGTTAAAGCGCTGCTGTTGATCGCAAGA 1417
DB 1350 CAGAAATGAGCTCAGCTAGTAGATTCCTCTGATGGGATCTTTGGTCTTGTACCGCAAA 1409
QY 1418 TATTGACGAGATTGGAAGCAACGACTACAACTTCAAGAGGAGGCTTATCTTAGCA 1477
DB 1410 TACTAGATGAGTTGAGCCATGACTACAACTTCAAGAGAGAGCATATGTGAGCA 1469
QY 1478 AGCCAAGAGCTCTCTACCTTGCCTTATGCAAAATCTCTTGTGCCCCCTAATA 1537
DB 1470 AATCAAGAAAGTTGATTGCTATACCTATTGCATATGCAAAATCTCTTGTGCTCTCTCAA 1529
QY 1538 GAATTCCTCTCCACTAGCAAGA 1561
DB 1530 AACTGCTCTCTTCAAGATAAA 1553
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RESULT 4
A21360 LOCUS A21360 1646 bp mRNA linear PAT 06-JUN-1994
DEFINITION L.esculentum pTOM5 mRNA.
ACCESSION A21360
VERSION A21360.1 GI:512395
KEYWORDS
SOURCE Lycopersicon esculentum.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
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EGMDLRSKRTKDELILYICYVAGTVGLMSVPIMGTAPESSKATTESVYNALALG
IANQLNILLRVDGEARRGRVYLPODELAQGLSDEIDFAGVTPDKWIRFMKQIHRA
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polya_site 1630
BASE COUNT 529 a 249 c 388 g 480 t
ORIGIN

Query Match 48.7%; Score 842; DB 6; Length 1646;
Best Local Similarity 74.3%; Pred. No. 1.5e-197;
Matches 1222; Conservative 0; Mismatches 330; Indels 92; Gaps 9;

QY	101	TATATGCTGTAATAGTGGATAGACTCTAGTGGATATCTAC----	AAGTATTGGTTTT	157
DB	53	TAATTTTGTAGAGTGGAAATATCTCTAGTGGAAATCTACTAGGAGTAATTTATTT		112
QY	158	TGATAAAATAGGCTGAGTGCAGAGGTAACATAAGGAAAGACAAACAACTTGGCAATTGT		217
DB	113	CTATAAACTAAGTAAGTTGGAGGTGACA-AAAGAAAGACAAAAATCTTGGAAATGT		171
QY	218	TTTAGACCCAGAGTTCTTGTTCATGAGCATGCTGTTGCTTGTGCTGTTGTTT		277
DB	172	TTTAGACAACCAAGT---TTTCTTGCTCAGATGCTGTTGCTTGTATGGTTGTTT		228
QY	278	CTCCACTTCCGAGTCTCGAATGGGACAGGATTTGGATTCAGTCCGAGAGGAAC		337
DB	229	CTC---CTTGTGAGCTCGAATGGGACAAAGTTTCATGGAATCAGTCCGGGAGGAAAC		285
QY	338	CGCTTTTGTATCATCCAGGTTCTAGCTCAGATAGGAATTCATGCTGGAATGGGAGAA		397
DB	286	GTITTTTGTATCATCAGG-----CATGGAATTTGGTGTCCAAATGAGAGAA		333
QY	398	TCAGAAAGAGTGGGACAGAAAGGTGGAATTTGGCTCTTTAATGCTGATCCCAAGATAT		457
DB	334	TCATAGAGGT-----		344
QY	458	CATGCTTGGTGGATCAAGAACTGAAAGGGAAGCACTTCTCTGTACATCCAGTTGG		517
DB	345	-----GGTGAAGAACAACTAATAATGAGCGGAAATTTCTGTACGGTCTGCTATTT		396
QY	518	TGGCTAGCCAGCTGGGAGAAATGACTGTGCATCAGAGAAAGGCTGATGATGCTGAT		577
DB	397	TGGCTACTCCATCTGGAGAACGGAGATGACATCGGAAACAGATGGTCTATGATGTTGTTT		456
QY	578	TAAAGCAGGAGCTTTAGTGAAGGAGGAGCTGAGATCTACCGATGATTTAGAAGTGAAGC		637
DB	457	TGAGGAGGAGGAGCTTGGTGAAGAGGCACTGAGATCTACCAATGAGTTAGAAGTGAAGC		516
QY	638	CGGATATTTGTTCCAGGAAATTTGGGCTTTGTGAGTGAAGCATATGATCGTTGGCG		697
DB	517	CGGATATACCTATTTCCGGGAAATTTGGGCTTTGTGAGTGAAGCATATGATAGTTGGTG		576
QY	698	AAGTATGTCAGAGTATGCAAGACATTTTACTTTAGGAACCAAGCTAATGACCCGACAGA		757
DB	577	AAGTATGTCAGAGTATGCAAGACGTTTAACTTTAGGAACATATGCTAATGACCTCCGAGA		636
QY	758	GAGAAGAGCTATCTGGGCAATATATGTTGGTGCAGGAGAACGGATGAGCTTTGTTGATG		817
DB	637	GAGAAGGAGCTATCTGGGCAATATATGTTGGTGCAGGAGAACGATGAACTTTGTTGATG		696
QY	818	GCCCTATGATCCCATCACTCCGCAAGCTTTAGATAGTGGGAGACCGAGCTGGAAG		877
DB	697	GCCCAACGCTATATATTTACCCCGCAGCTTAGATAGTGGGAAATAGGCTAGAG		756
QY	878	ATATTTTCACTGGGCGCCATTTGATATGCTGATGCTGCTTTATCCGATACTGTCCTCA		937
DB	757	ATGTTTTCAATGGGCGCCCAATTTGACATGCTCGATGTTGCTTTGTCGCGATACAGTTCTTA		816

QY	938	GATTTCCTGTTGATATTCAGCCATTCAGAGATATGATTGAAGGAATCGTATGACCTGT	997
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QY	998	GGAATCCAGATCAAAACCTTTGATGAGCTATATCTCTATTGTTACTATCTTCTGCTGA	1057
DB	877	GAAATTCAGATCAAAACCTTCGACGAATATACCTTTATTGTTATTATCTTCTGCTGA	936
QY	1058	CTGTAGGATTCAGAGTTCCTCAGTTATGGTATGCTGACCTGAATCAAGGCAACAACAG	1117
DB	937	CGGTGGTGTGATGAGTTCCTCAATATGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCT	996
QY	1118	AGAGTGTATATATGCTGCTTTTGGCTTTAGGGCTTGCCTGCTGCTGCTGCTGCTGCTGCT	1177
DB	997	AGAGCTATATATGCTGCTTTTGGCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1056
QY	1178	GAGATGAGGAGAGATGCTGAGAGAGAGATATCTTCCCTCAAGATGAATTAGCAC	1237
DB	1057	GAGATGTTGAGAGAGATGCTGAGAGAGAGAGTCTACTTGCCTCAAGATGAATTAGCAC	1116
QY	1238	AGCAGGCTCTCCGACGAGACATATTTGCTGGAAGAGTCACTATAGTGGAGAACT	1297
DB	1117	AGCAGGCTCTATCGATGAGATATATTTGCTGGAAGAGTCACTATAGTGGAGAACT	1176
QY	1298	TTATGAAGAAACAAATTCAGAGGCGAGGAAATTTCTTTGATGAGTCAGAGAAAGGTGCA	1357
DB	1177	TTATGAAGAAACAAATACATAGGCGAGAGAGTTCTTTGATGAGGAGAGAAAGCGTGA	1236
QY	1358	CAGAACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1417
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QY	1418	TATGAGGAGATTTGAGCCCAACACTACACAACTTCACAGAGGAGGCTTATGTTAGCA	1477
DB	1297	TACTGATGAGTTGAGCCCAACACTACACAACTTCACAGAGAGAGCATATGTTAGCA	1356
QY	1478	AGCCAAAG-AAGCTTCTCAGCTTCCCTTCTTATGCAAAATCTTTGTCCTCCCTAAT	1536
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QY	1537	AGAACTTCTCTCCACTGAGCAAGACATGAAATGAGTGTGAGTCAATGATATATATAC	1596
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DB	1537	CATAAATATTAGTTGTTGATTAACATTCATATATATATATATCTCTTGTAGTTGTTATCTC	1596
QY	1705	ACACTCATCAACCTCAAGTGAG 1728	
DB	1597	ACTTATCTCAACTCTTTTGAGAG 1620	

RESULT 5
AR007503
LOCUS
DEFINITION
Sequence 2 from patent US 5750865.
AR007503
ACCESSION
AR007503.1
VERSION
GI:3966987
KEYWORDS
Unknown.
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1646)
AUTHORS
Bird,C.Roger., Grierson,D. and Schuch,W.Walter.
TITLE
Process for modifying the production of carotenoids in plants, and
DNA, constructs and cells therefor
JOURNAL
Patent: US 5750865-A 2 12-MAY-1998;

SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 1239)
AUTHORS Drake, C.R., Bird, C.R. and Schuch, W.W.
TITLE ENHANCEMENT OF GENE EXPRESSION
JOURNAL Patent: WO 97/46690-A 2 11-DEC-1997;
ZENECA LTD (GB)
FEATURES
source Location/Qualifiers
1. 1239
/organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
/clone="G70M5 - PHYTOENE SYNTHASE GENE"
BASE COUNT 377 a 207 c 317 g 338 t
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Query Match 46.9%; Score 811.2; DB 6; Length 1239;
Best Local Similarity 79.0%; Pred. No. 6.5e-190;
Matches 1035; Conservative 0; Mismatches 203; Indels 72; Gaps 3;
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DB 1 ATGCTGTTGCTTGTGGTGTCTCCACTCCGAGGTCCTGAATGGGACAGGA 57
QY 310 TTGTTGGATTCAGTCCGAGAGGAACCGCGTCTTTGTATCATCCAGGTTCTAGCTCGA 369
DB 58 TTATGGAATCAGTCCGGGAGGAAACCGTTTTTGTATTCATCGAGG 105
QY 370 GATAGGAATTCAGTGGGAGGAGATCAAGAAAGTGGGACAAAGGTGGAAATTT 429
DB 106 CATAGGAATTTGGTGTCAATGAGAGAAATCAATAGAGT 144
QY 430 GGCTCTTAATGCTGATCCCAAGATATTCATGCTGGGTGGATCAAGAACTGAAAGGGA 489
DB 145 -----GTGGAAAGCAAACTAATANTGGA 168
QY 490 ACCACTTCTCTGTACATCCAGTTTGGTGGCTAGCCAGCTGGAGAAATGACTGTGTCA 549
DB 169 CGGAAATTTCTGTACGCTGTCTATTTTGGCTACTCCATCTGGAGAACGGACGATGACA 228
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DB 229 TCGGAACAGATGGTCTATGATGTGTTTGGAGGAGGAGCGCTTGGTGAAGAGGCACTG 288
QY 610 AGATCTACCGATGATTTAGAGTGAAGCGGATATTTGTTCCAGGGAATTTGGGCTTG 669
DB 289 AGATCTACCAATGATTTAGAGTGAAGCGGATATACCTATTTCCGGGGAATTTGGGCTTG 348
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DB 349 TTGAGTGAAGCATATGATGATGTGTTGAGAGTATGTGAGAGATATGCAAGACGTTTAA 408
QY 730 TTAGAACCAAGCTAATGACCCAGAGAGAGAGAGCTATCTGGGCAATATATGTGTTGG 789
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QY 790 TCAGAGAACCGATGAGCTTGTGATGCCCTATATGATCCCATTAATCCCGCAAGCT 849
DB 469 TCAGAGAACCAAGATGAACTTGTGATGCCCAAGCATCATATATTTACCCCGCAGCC 528
QY 850 TTATAGTGGGAGACAGGCTGGAAGATATTTTCAATGGGCGCCATTTGATATGTT 909
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QY 910 GATGCTGCTTTATCCGATCTCTCCAGATTTTCTGTTGATTTATTCAGCCATTCAGAGAT 969
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RESULT 8
ARI56064 1239 bp DNA linear PAT 08-AUG-2001
LOCUS ARI56064
DEFINITION Sequence 2 from patent US 6239331.
ACCESSION ARI56064
VERSION ARI56064.1 GI:15124117
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1239)
AUTHORS Drake, C. Rachel., Bird, C. Roger. and Schuch, W. Walter.
TITLE Enhancement of tomato phytoene synthase gene expression with a modified DNA
JOURNAL Patent: US 6239331-A 2 29-MAY-2001;
FEATURES Location/Qualifiers
source 1. 1239
BASE COUNT 377 a 207 c 317 g 338 t
ORIGIN
Query Match 46.9%; Score 811.2; DB 6; Length 1239;
Best Local Similarity 79.0%; Pred. No. 6.5e-190;
Matches 1035; Conservative 0; Mismatches 203; Indels 72; Gaps 3;
QY 250 ATGCTGTTGCTTGTGGTGTCTCCACTCCGAGGTCCTGAATGGGACAGGA 309
DB 1 ATGCTGTTGCTTGTGGTGTCTCCACTCCGAGGTCCTGAATGGGACAGGA 57
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Db 106 CATAGGAATTTGGTGTCAATGAGAGAAATCAATAGAGT 144
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QY 490 ACCACTTCTCTGTACATCCAGTTTGGTGGCTAGCCAGCTGGAGAAATGACTGTGTCA 549
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Db	491	ATGTGAACCCAGATATGCTTTACCGGAACCTTTAAGTCTCTCAGTGAAGCTTATGATC	550
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Db	551	GTTGTGGAGAAGTTTGGCGCGAGTAGTCTAAGACACATTTTACTTGGGAACCTTGTCTGATGA	610
Qy	749	CCCCAGAGAGAGAAGAGCTATCTCGGCCAATATATGTGTGTGCAGAGAACGGATGAGC	808
Db	611	CTCTCTAAAGGGCGAAGGGCTATATGGGCTATATATGTGTGTGTAGGAGACAGATGAGC	670
Qy	809	TTGTTGATGGCCCTAATGATCCCAACATAAAGTCGCAAGCTTTAGATAGTGGGAGACCA	868
Db	671	TCGTTGATGGCCCTAATGCTTCACACATTAATCCACAGCTTTAGACAGTGGGGAGTCCA	730
Qy	869	GGCTGGAAGATATTTTCAAGTGGCGGCCCATTTGATATGCTGTGCTCTTTATPCGATA	928
Db	731	GGTTGGAAGACCTTTTTCGGGGCTGCTCCATTTGATATGCTTGATGCTGCATTATCAGATA	790
Qy	929	CTGCTCCAGATTTCTCTGTTGATATTCAGCCATTTCAGAGATATGATTCGAAGGATCGTA	988
Db	791	CAGTACCACAAATTTCTGTCTGCACATTCAGCCATTTCAGAGATATGATAGAAGGAATGAGA	850
Qy	989	TGGACTTGTGGAATCCAGATACAAACCTTTTCGATGAGCTATATCTCTATTTGTTACATG	1048
Db	851	TGGACCTTAGGAAGTCAAGATACAAACCTTTTGATGAATTATCTGTATTTGTTATATG	910
Qy	1049	TTGCTGGTACTGTAGGATGATGAGTGTTTCAGTTATGGGTATTGCACTGGAATCAAAGG	1108
Db	911	TTGCTGGGACCGTAGGGCTAATGAGTGTTTCCAGTTATGGCATATGGCACTGCACTGACAGG	970
Qy	1109	CAACAACAGAGAGTGTATATAATGCTGCTTTGGCTTTTAGGCTTTGCAAAATCAACTRACCA	1168
Db	971	CAACAACAGAGCGTCTACAATGCAGATTCGCACTAGGGAATGCTTAATCAGCTCACTA	1030
Qy	1169	ATATACTCAGAGATGTAGGAGAAGATGCCAGAAGAGGAAGTAGTATCTTGCCCTCAAGATG	1228
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Qy	1229	AATTAGCACAGCAGGCTCTCCGACGAGAGACATATTTGCTGGAGAGTGNACTGATAGT	1288
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Qy	1349	AAGGTGTCACAGACTGGACTCTGCTAGTAGATGCCCTGTGTTAACAGCGCTGCTGTGTG	1408
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Qy	1409	ATCGCAAGATATTGGACAGAGATTGAAGCCACGACTACAAACCTTCACAGAGAGGCGTT	1468
Db	1271	ACCGGCAAACTCTGGATGAGATTGAGGCCAATGATTACAAACCTTCACAAAGAGAGCTT	1330
Qy	1469	ATGTTAGCAAGCCAAGAGCTTCTCACCTTGCCCATTTGCTTATGCAAAATCTCTTGTGC	1528
Db	1331	ATGTGAGTAAAGCCAAAGAGATAGTGCACCTACCAATTCGATATGCAAAATCCCTCTTAC	1390
Qy	1529	CCCTTAATAGAA	1540
Db	1391	GCCCGTCAAGAA	1402

RESULT 12	AB037975	AB037975	1689 bp	mRNA	linear	PLN 25-NOV-2000
LOCUS	AB037975	Citrus unshiu mRNA for phytoene synthase, complete cds.				
DEFINITION	AB037975					
ACCESSION	AB037975.1	GI:11344506				
VERSION	AB037975.1	GI:11344506				
KEYWORDS		phytoene synthase.				
SOURCE		Citrus unshiu (cultivar:Satsuma mandarin)				
		mature stage pulp				
		cDNA to				
		mRNA.				

ORGANISM Citrus unshiu
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.
1 (sites)
AUTHORS Ikoma,Y., Komatsu,A., Kita,M., Ogawa,K., Omura,M., Yano,M. and
Moriguchi,T.
TITLE Expression of a phyton synthase gene and characteristic carotenoid
accumulation during citrus fruit development
JOURNAL Physiol. Plantarum 111, 232-238 (2001)
AUTHORS 2 (bases 1 to 1689)
Moriguchi,T.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Takaya Moriguchi, National Institute of
Fruit Tree Science, Department of Research Planning and
Coordination; 2-1 Fujimoto, Tsukuba, Ibaraki 305-8605, Japan
(E-mail: takaya@fruit.affrc.go.jp, Tel:81-298-38-6416,
Fax:81-298-38-6437)
FEATURES Location/Qualifiers
source 1..1689
/organism="Citrus unshiu"
/cultivar="Satsuma mandarin"
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LGLTMSERRIAIWIYVCMRTDYLVDGPNASHIITPALTDRWESRLDFRGRPD
MCLDASDTVTFPVDIQPFPRDMIEGRMDLRKRYNDFELYLYCYVYAGTVGLMS
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BASE COUNT 512 a 302 c 388 g 487 t
ORIGIN
Query Match 40.3%; Score 696.8; DB 8; Length 1689;
Best Local Similarity 71.2%; Pred. No. 1.3e-161;
Matches 949; Conservative 0; Mismatches 377; Indels 6; Gaps 2;
QY 212 AATTGTTTATAGACCACCGAGTTCTTGTTTCATGCACATGTCGTGTTGCTTTGTTGGG 271
Db 141 AAAATTTCTTTTATCCAAAATAATAATATTTTACACACATGCTGTTACATGCTGTGGG 200
QY 272 TTGTTTCTCCACCTTCGAGGCTCTCGAATGGGACGAGATTGTTGATTTCAGTCGAGAAG 331
Db 201 TTGTATCACCTACTACATTTGCCAATTTGCTTCGGGTTGCTGCATTCAGTTTCGAGAGG 260
QY 332 GAAACCGCGTCTTTGTATCATCCAGGTTCCCTAGCTCGAGATAGGAATTTGATCTGGAATG 391
Db 261 AAAACAGCGTGTTTTATTTCATCAAGATTTCTTTACCAACATCAAAACCCGGACTCTCTGT 320
QY 392 GGAGAATCAGAAGGTGGGACACAAGGTGGAAATTTTGCTCTTTAATTCGTGATCCAA 451
Db 321 TTAATTCAGACCTTAAGCAGCTTAATAATAGTAATAAGACAGACGGAATTTCTATCCTT 380
QY 452 GAVATTTCATGCTTGGGTGGATCAAGAACTGAAAAGGGGAAGCACTTCTCTGTATCAGTCCA 511
Db 381 TAGTACAGATTGAGGCATCCTTGCTC --- ACTGTGAATCGACTTCGCTTGAATATCAT 437
QY 512 GTTTGTGGGTAGCCAGCTGGGAAATGACTGTGTTCATCAGAGAAAAGGTGTGATGATG 571
Db 438 GTATGGTTGTAGCACTGCTGGAGAGTGGCCATGCTCTTCAGAGAATGTTTACATG 497
QY 572 TGGTATTAAAGCAGGCGAGCTTTAGTGAAGAGGCGAGCTGAGAT --- CTACCGATGATTTAG 638
Db 498 TTGTGCTCAAGCAGGCGAGCTTGTGTTAATGAACAACCAAGTGGGGTTTACTCGTCTGTTG 557

QY	629	AAGTGAAGCCGGAGATATGTGTTCCAGGAAATTTGGGCTTGTCAGTGAAGCATATGATC	688
DB	558	ATGTGAACCCAGATATTCGTTTACC CGGAACCTTTAAAGTCTGCTCAGTGAAGCTTATGATC	617
QY	689	GTGTGCGCAAGTATGTGCAGAGTAGCAAAAGACATTTTACTTAGGAACCAAGCTATGA	748
DB	618	GTGTGGAGAAAGTTTGGCCCGAGTAGCTAGACATTTTACTGGGAACCTTGCTGTATGA	677
QY	749	CCCCAGAGAAAGAAAGAGCTATCTGGCAATATATGTGTGTCAGAGAAACGGATGAGC	808
DB	678	CTCTCAAGCGAAGGGCTATATGGGCTATATATGTGTGCTAGGAGNACAGATGAGC	737
QY	809	TTGTTGATGGCCCTTAATGCATCCACATACTCCGCAAGCTTTAGATAGGTGGGAGACCA	868
DB	738	TCGTTGATGGGCTTAATGCTTCACACATAACTCCAACAGCTTTAGACAGGTGGGAGTCCA	797
QY	869	GGCTGGAACATATTTTCAGTGGGGCGGCATTTGATATGCTTGATGCTGCTTTATCCGATA	928
DB	798	GGTGTGAAGACCTTTTCGGGGTGTCTCATTTGATGTGCTTGATGCTGCATTTATCAGATA	857
QY	929	CTGCTCCAGATTTCTCTGTGTATTTTCAGCCATTCAGAGATATCATTTGAAGGAATGCGTA	988
DB	858	CAGTACCAAAATTTCTCTGTCGACATTCAGCCATTCAGAGATATCATAGAGGAATGAGGA	917
QY	989	TGGACTGTGGAAATCCAGATACAAAACCTTCGATGAGCTATATCTCTATTGTTACTATG	1048
DB	918	TGGACCTTAGGAAGTCAAGATACAAAACCTTTGATGAATTACTTGTTATTATTATG	977
QY	1049	TTGCTGCTACTGTAGAGATTGATGAGTGTCCAGTTATGGGTATTTCACCTTGAATCAAGG	1108
DB	978	TTGCTGGGACCGTAGGGCTTAATGAGTGTTCAGTTATGGGCATAGCACCCTGACTCACAGG	1037
QY	1109	CAACAACAGAGAGTGTATATATGCTGCTTTGGCTTTTAGGCTTTGCAAAATCAACTAACCA	1168
DB	1038	CAACAACAGAGAGCGCTACATATGCAGCATTTGGCNACTAGGAGATTGCTAATCAGCTCACTA	1097
QY	1169	ATATACTCAGAGATGTAGGAGAAGATGCCAGAAGAGAGATATACTTGCCCTCAAGATG	1228
DB	1098	ACATACTCAGAGATGTTGGAGAGAGTGGCCGAAGAGGAAGGGTTATCTACCAACAAGATG	1157
QY	1229	AATTAGCACAGCAGGGCTCTCCGACGAGAGACATATTTGCTGGAGAGTGNACTGATTAAGT	1288
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DB	1278	ACGGTGTACCGAGCTGAGTGAAGCTAGTCGATGGCCGGTATGGCTTCATTGCTGTGTG	1337
QY	1409	ATCGAAGATATTGGACGAGATTGAAGCCACGACTACAACTACCAAGGAGGGCTT	1468
DB	1338	ACCGGCAATATCTGGATGAGATTGAGGCCATGATTACACAACCTTCACAAGAGAGCTT	1397
QY	1469	ATGTTAGCAAGCCAAAGAGCTTCTCACCTTGCCCATTTGCTTATATGCAAAAATCTCTTGTC	1528
DB	1398	ATGTGAGTAAAGCCAAAGAGATAGTGCACATACCAATTTGCATATGCAAAATCCCTCTTAC	1457
QY	1529	CCCTTAATGAA	1540
DB	1458	GCCCGTCAAGAA	1469

RESULT 13	
AF152892	
LOCUS	1773 bp mRNA linear PLN 04-APR-2001
DEFINITION	Citrus x paradisi phytoene synthase mRNA, complete cds.
ACCESSION	AF152892
VERSION	AF152892.2 GI:13542331
KEYWORDS	.
SOURCE	Citrus x paradisi.

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Db 658 ACTTTAAGTCTGCTCAGTGAAGCTTATGATCGTTGTGGAGAGTTTGGCGCGATATGC 717
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Db 838 AACTCCACAGCTTTAGACAGTGGGAGTCCAGGTTGAGAGACCTTTTCGGGGTCAGCC 897
QY 897 ATTGATATGCTGATGCTGCTTTATCCGATACTCTCCAGATTTCTCTGTTGATATCA 956
Db 898 ATTGATATGCTGATGCTGCTATATACAGTACAGTAAACCAATTTCTGTCGACATCA 957
QY 957 GCATTCAGAGATATGATTAAGGATGCGGTATGACCTGTGGAAATCCAGATCAAAAAC 1016
Db 958 GCATTCAGAGATATGATTAAGGATGAGGATGAGGATGACCTTAGGAAGTCAAGATCAAAA 1017
QY 1017 TTTCGATGAGCTATATCTATTGTTACTATGCTGTGCTAGTGGATTTGATGAGTGT 1076
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QY 1377 TAGATGCTGCTGTTAAGCAGCGCTGCTGTTGATCGCAAGATATTGGACGAGATTGAAGC 1436
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QY 1437 CAACGACTACAACAACTTCACAGGAGGCTTATGTTAGCAAGCCAAAGAGCTTCTCTAC 1496
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RESULT 14
E15683
LOCUS E15683 Gentiana lutea mRNA for Phytoene synthase 4, complete cds.
DEFINITION Gentiana lutea mRNA for Phytoene synthase 4, complete cds.
ACCESSION E15683
VERSION E15683.1 GI:5710366
KEYWORDS JP 1998084966-A/4.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2868)
AUTHORS Koiba, H., Kobayashi, H. and Yamamura, S.
TITLE NEW PHYTOENE SYNTHASE GENE
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JOURNAL Patent: JP 1998084966-A 4 07-APR-1998;
COMMENT IWATE, PREP GOV
OS Gentiana lutea
PN JP 1998084966-A/4
PD 07-APR-1998
PF 17-SEP-1996 JP 1996245107
PI KOIBA HIROYUKI, KOBAYASHI HITOSHI, YAMAMURA SABURO PC
C12N15/09,C07H21/04,C12N9/00/C09B61/00.(C12N9/00,C12R1:91); CC
Strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..2868
FH /organism='Gentiana lutea'
FH /tissue_type='petal'
FH CDS 400..1689
FH /product='phytoene synthase 4'.
FEATURES
Source Location/Qualifiers
Source 1..2868
/db_xref='taxon:32644'
BASE COUNT 887 a 499 c 648 g 833 t 1 others
ORIGIN
Query Match 40.1%; Score 692.4; DB 6; Length 2868;
Best Local Similarity 73.6%; Pred. No. 1.5e-160;
Matches 949; Conservative 0; Mismatches 311; Indels 30; Gaps 4;
QY 240 TTTCATGAGCATGCTCTGTTGCTTTGTTGGTGTGTTTCTCCACCTTCGAGGCTCGAA 299
Db 390 TTCTGTTACATGCTCTATTTGTACGTAATGTTGTTGCGCGAGTCTGGAAGTTTGAG 449
QY 300 TGGGACAGGATTTGGATTTCAGTCCGAGAGAAACCGCTCTCTGTATCATCCAGTT 359
Db 450 TGGCAATGTTTCTTGGAGCCAATTCGAGAAAGTTACCATTTTTCG----- 495
QY 360 CCTAGCTCAGATAGGAATTTGATGGAATGGGAGAAATCAAGAAAGTTGGGAGACAAAG 419
Db 496 -----GATAAAAGTTTAATGTACAAATGGAAGAGTTAAGAAAGTAGACACCAAG 545
QY 420 GTGGAATTTGCTCTTTAATGCTGATCAAGATATTCATGCTGGTGGTGATCAAGAAC 479
Db 546 GCGTATGATCAGCTTATGGGTTGGAGATTTGATGCTCATTTGCTTGAGAGAGTCTGATT 605
QY 480 TGAAG---AGGGAAGCAGCTTCTCTACAGTCCAGTTTGGTGGCTAGCCAGCTGAGAG 536
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QY 537 AATGACTGCTCATCAGAGAAAAGGTGATGTTGTTGTTAATGAGCAGGACGCTTTAGT 596
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QY 597 GAAGAGGACGCTGAGATCTACCGATGATTTAGAAGTGAAGCCGATATTTGTTCTCCAG 656
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QY 657 GAATTTGGGCTTTGTTGAGTGAAGCATATATGATCGTTGCGGAGAGTATGTGAGAGTATGC 716
Db 786 AAACGCGAAGCTGTTGAATGAAGCTTATGATCGTGTGAGAGAGTATGTCTCAATATGC 845
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QY 777 AATATATGCTGCTGAGGAGAACGATGAGCTTTGTTGAGCCCTAATCATCCACACAT 836
Db 906 GATATATGATGCTGTTAGGAGGACATGAGCTTTGTTGAGCCCTAAGCCGCTACACAT 965
QY 837 AACTCCGCAAGCTTTAGATAGTGGGAGACAGGCTGGAAGATATTATTCAGTGGCGGCC 896
Db 966 AAATCCCAACCGGTTAGATAGTGGGAGCAAGATTTAGAGATGTTTTTCAAGGCAACC 1025
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